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(54) Title: CHIMERIC PRE-ACTIVATED TRANSCRIPTION FACTORS (57) Abstract <p>Disclosed herein is a chimeric protein comprising a pre-activated transcription factor and a strong transcription activation domain for regulating fungal gene expression, and reagents and methods for constructing and using said protein.</p>		

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CHIMERIC PRE-ACTIVATED TRANSCRIPTION FACTORS

Background of the Invention

5 Fungal species are the commercial source of many medicinally useful products, such as antibiotics (e.g., beta-lactam antibiotics such as penicillin, cephalosporin, and their derivatives), anti-hypercholesterolemic agents (e.g., lovastatin and compactin), immunosuppressives (e.g., cyclosporin), and antifungal drugs (e.g., pneumocandin and echinocandin). All
10 of these drugs are fungal secondary metabolites, small secreted molecules that fungi utilize against competitors in their microbial environment. Fungi also produce commercially important enzymes (e.g., cellulases, proteases, and lipases) and other products (e.g., citric acid, gibberellic acid, natural pigments, and flavorings).

15 The production of secondary metabolites, enzymes, and other products is regulated by coordinated gene expression. For example, the production of penicillin is limited by the activity of two enzymes, encoded by the *ipnA* and *acvA* genes. PacC, a zinc-finger transcription factor, binds to sequences upstream of these two genes. Moreover, increased activity of PacC
20 leads to both increased enzyme activity and penicillin production.

Our understanding of transcriptional regulation of secondary metabolite production, as exemplified above, has increased greatly over the past decade. To date, however, the use of genetically-engineered transcription factors has not been applied to increase production of commercially-important
25 fungal products. In contrast, methods to increase production of penicillin currently rely upon mutagenesis and selection for mutants which display increased secondary metabolite production.

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Summary of the Invention

The invention provides a means to increase the production of secondary metabolites in fungi by genetic manipulation of the fungal organism itself. The ability to increase fungal secondary metabolite production has at least two important applications. First, it will allow increased production of existing secondary metabolites which are useful in clinical and experimental settings. Second, increasing production of secondary metabolites will facilitate identification of new compounds in fungi that otherwise make undetectable levels of these compounds in the laboratory.

Accordingly, in one aspect, the invention features a two-part chimeric transcription factor including (i) a pre-activated transcription factor functional in a fungal strain, and (ii) a transcription activation domain that is different from the transcription activation domain naturally associated with the transcription factor. In a preferred embodiment, the transcriptional activity of the chimeric transcription factor is greater than the transcriptional activity naturally associated with the pre-activated transcription factor. In another preferred embodiment, the pre-activated transcription factor is pre-activated by truncation. In a related preferred embodiment, the pre-activated transcription factor includes a substitution of a serine or threonine residue with an alanine, aspartic acid, or glutamic acid residue, wherein the substitution pre-activates the transcription factor (e.g., by mimicking or otherwise altering phosphorylation). In another preferred embodiment, the transcription factor is a member of the PacC family (defined below) and can be pre-activated. In a related preferred embodiment, the pre-activated transcription factor contains portions of the amino acid sequence shown in Fig. 1 (SEQ ID NOs: 1-6).

In another aspect, the invention features a vector including DNA encoding a chimeric transcription factor including (i) a pre-activated

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transcription factor functional in a fungal strain, and (ii) a transcription activation domain that is different from the transcription activation domain naturally associated with the transcription factor. The DNA is operably linked to a promoter capable of directing and regulating expression of the chimeric
5 transcription factor in a fungal strain.

The transcription factor encoded within the vector described above is expressed in a fungal cell, such as a filamentous fungal cell, which produces the secondary metabolite of interest and in which expression of the transcription factor increases the production of the secondary metabolite by the
10 cell. The secondary metabolite can be non-proteinaceous or it can be a protein or peptide.

In another aspect, the invention features a method of producing a secondary metabolite of interest, including the steps of (i) introducing into a fungal cell, such as a filamentous fungal cell, a vector including a promoter capable of controlling gene expression in the fungal cell, and a nucleic acid
15 encoding a two-part transcription factor including a DNA-binding domain and a transcription activation domain; and (ii) culturing the fungal cell under secondary metabolite-producing conditions. In a preferred embodiment, the transcription activation domain is different from the transcription activation
20 domain naturally associated with the DNA-binding domain. In other preferred embodiments, the transcription factor is a pre-activated transcription factor (pre-activated by substitution of a serine or threonine residue with an alanine, aspartic acid, or glutamic acid residue, or pre-activated by truncation). In other preferred embodiments, the DNA binding domain of the transcription factor is
25 from a fungal transcriptional activator or from a fungal transcriptional repressor.

By "pre-activated transcription factor" is meant a transcription factor

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or fragment thereof that, compared to the precursor molecule, is capable of 1) increased binding, either direct or indirect, to a specific DNA sequence located in a gene regulatory region (e.g., a promoter), or 2) increased transcription activating properties. Pre-activated transcription factors may be able to activate transcription from promoters, but this is not necessarily the case. For example, a transcription factor DNA-binding domain with binding properties but no transactivation activity is considered to be a pre-activated transcription factor. "Pre-activation by truncation" or "pre-activated by truncation" means that removal of a portion of the protein leads to pre-activation. This occurs *in vivo* through proteolytic cleavage. In the invention, pre-activation by truncation is achieved with the use of DNA that encodes a pre-activated form of the protein, excluding portions of the protein that would be proteolytically cleaved *in vivo*.

By "substantially identical" is meant a polypeptide or nucleic acid exhibiting at least 50%, preferably 85%, more preferably 90%, and most preferably 95% identity to a reference amino acid or nucleic acid sequence. For polypeptides, the length of comparison sequences will generally be at least 16 amino acids, preferably at least 20 amino acids, more preferably at least 25 amino acids, and most preferably 35 amino acids. For nucleic acids, the length of comparison sequences will generally be at least 50 nucleotides, preferably at least 60 nucleotides, more preferably at least 75 nucleotides, and most preferably 110 nucleotides.

By "promoter" is meant a sequence sufficient to direct and/or regulate transcription. Also included in the invention are those elements which are sufficient to render promoter-dependent gene expression controllable for cell type-specific, tissue-specific, temporal-specific, or inducible by external signals or agents; such elements may be located in the 5' or 3' or intron

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sequence regions of the native gene.

By "operably linked" is meant that a gene and one or more regulatory sequences are connected in such a way as to permit gene expression when the appropriate molecules (e.g., transcriptional activator proteins) are bound to the regulatory sequences.

Other features and advantages of the invention will be apparent from the following description of the preferred embodiments thereof, and from the claims.

Drawing

Fig. 1 is an alignment of the zinc-finger DNA-binding domain of PacC family members from *Aspergillus nidulans* (SEQ ID NO: 1), *Aspergillus niger* (SEQ ID NO: 2), *Penicillium chrysogenum* (SEQ ID NO: 3), *Yarrowia lipolytica* (SEQ ID NO: 4), *Candida albicans* (SEQ ID NO: 5), and *Saccharomyces cerevisiae* (SEQ ID NO: 6). Identity is represented by shaded regions; similarity is represented by boxed regions.

Detailed Description

The invention features a two-part chimeric protein including a pre-activated transcription factor and a strong transcription activation domain for regulating fungal gene expression. The protein is encoded by nucleic acids operably linked to a strong promoter in a vector which allows for expression in fungal cells. The effect of the transcription factor is to facilitate expression of a protein which itself is a desired product, or which acts as an element (e.g., an enzyme) by which a desired product is made by the host fungal cell. Each of these components is described below. Experimental examples described herein are intended to illustrate, not limit, the scope of the claimed invention.

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Pre-Activated Transcription Factor

The vectors of the invention can include DNA encoding any proteinaceous transcription factor that can be provided in pre-activated form; i.e., the vector encodes the protein in a form in which it is already activated; i.e., no post-translational processing is required for the protein to be active in a fungal cell to bind to regulatory DNA of the cell to facilitate gene expression.

Transcription factors regulate the level of gene expression by affecting the activity of the core transcriptional machinery at the promoter of each gene. Several mechanisms have evolved to control the activity of transcription factors.

Post-translational modification is one mechanism by which transcription factors are regulated. Proteolytic cleavage is one post-translational mechanism for regulating the activity of a transcription factor (e.g., Pahl and Baeuerle, *Curr. Opin. Cell Biol.*, 1996, 8:340-347; Goodbourn and King, *Biochem. Soc. Trans.*, 1997, 25:498-502; Fan and Maniatis, *Nature*, 1991, 354:395-398). The fungal PacC family of transcription factors is one class of proteins that can be activated by proteolysis. Activating mutations have been described for PacC family members (see below); these mutations truncate the encoded protein, resulting in the production of a pre-activated form of the transcription factor.

Another method for pre-activating a transcription factor is to mimic the modifications which normally regulate its activity. For example, phosphorylation has been shown to positively regulate the activity of some transcription factors and negatively regulate that of others (see review by Hunter and Karin, *Cell*, 1992, 70:375-387). Other forms of post-translational modifications that can increase the activity of transcription factors include acetylation (Gu and Roeder, *Cell*, 1997, 90:595-606) and alkylation (e.g.,

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methylation)(Chinenov et al., *J. Biol. Chem.*, 1998, 273:6203-6209; Sakashita et al., *J Biochem (Tokyo)*, 1995, 118:1184-1191).

Dephosphorylation of particular residues can increase the activity of many transcription factors. Phosphorylation most commonly occurs on serine (Ser), threonine (Thr), and tyrosine (Tyr) residues; in some instance residues such as aspartate (Asp) and histidine (His) can be phosphorylated. The coding sequence for the phosphorylated residue can be mutated to encode an amino acid that cannot be phosphorylated and does not have a negatively charged side chain (e.g., alanine (Ala)). Ser→Ala, Thr→Ala, Tyr→Ala, and Asp→Ala substitutions are frequently used in the art to produce a pre-activated transcription factor (see, for example, Chen et al., *Proc. Natl. Acad. Sci. U.S.A.*, 1998, 95:2349-2354; Song et al., *Mol. Cell Biol.*, 1998, 18:4994-4999; O'Reilly et al., *EMBO J.*, 1997, 16:2420-2430; Hao et al., *J. Biol. Chem.*, 1996, 271:29380-29385).

Phosphorylation can also increase the activity of a transcription factor. Mutations of Glu or Asp for Ser, Thr, or Tyr are frequently used in the art to mimic a phosphorylation event and pre-activate a transcription factor (see, for example, Hoeffler et al., *Nucleic Acids Res.*, 1994, 22:1305-12; Hao et al., *supra*). Mutations that result in a substitution of Glu for Asp, at Asp residues which can be phosphorylated, can also cause activation (Klose et al., *J. Mol. Biol.*, 1993, 232:67-78; Krems et al., *Curr. Genet.*, 1996, 29:327-34; Nohaile et al., *J. Mol. Biol.*, 1997, 273:299-316).

Other mutations can be made that mimic activating post-translational modifications. For example, the *E. coli* Ada transcription factor is activated by methylation of cysteine (Cys) residue 69. A Cys→His substitution was found to result in activation (Taketomi et al., *Mol. Gen. Genet.*, 1996, 250:523-532). This particular substitution was identified by substituting Cys 69 with each of

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the other nineteen amino acids. Alternatively, in instances where no obvious substitution can be made to mimic a modification (e.g., acetylation), a random mutagenesis is performed to identify constitutively active forms of transcription factors (see, for example, Onishi et al., *Mol. Cell Biol.*, 1998, 18:3871-3879).

- 5 This technique can employ simple and rapid phenotypic or reporter selections, such as those described herein, to identify activated forms. For example, a *Saccharomyces cerevisiae* strain containing a reporter construct can be used to select for activated forms. Specifically, the *ipnA* promoter (P_{ipnA}) from *Aspergillus nidulans* may be fused to a gene from *Saccharomyces cerevisiae* that confers a growth advantage, such as *HIS3*, when PacC is pre-activated by a mutation. A P_{ipnA} -*HIS3* fusion has the added advantage that expression levels can be titrated by the compound 3-aminotriazole (3-AT). 3-AT is a competitive inhibitor of His3 that, when present in sufficient amounts, will inhibit the His3 expressed from P_{ipnA} and prevent this strain from growing on
- 10 SC-HIS. In this example, *pacC* coding sequence can be randomly mutagenized and vectors containing the mutated alleles are transformed into the reporter strain. Growth of a strain containing P_{ipnA} -*HIS3* only occurs on SC-HIS+3-AT plates when P_{ipnA} -*HIS3* expression is increased to overcome the competitive inhibition of His3 by 3-AT. This method provides a rapid technique for
- 15 screening for mutations which pre-activate a transcription factor.
- 20

The PacC Family of Transcription Factors

- One group of transcription factors useful in the invention are members of the PacC family. The PacC transcription factors regulate gene expression in response to changes in ambient pH. Members of the family have
- 25 the following characteristics: 1) They display significant (at least 35%) amino acid sequence identity to the *Aspergillus nidulans* PacC protein (Tilburn et al.,

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- EMBO J.*, 1995, 14:779-790). Such proteins have been identified in *Yarrowia lipolytica* (YlRim101p; Lambert et al., *Mol. Cell. Biol.*, 1997, 17:3966-3976), *Penicillium chrysogenum* (Suarez and Penalva, *Mol. Microbiol.*, 1996, 20:529-540), *Aspergillus niger* (MacCabe et al., *Mol. Gen. Genet.*, 1996, 250:367-374),
- 5 *Saccharomyces cerevisiae* (Inv8/Rim101/Rim1; Su and Mitchell, *Nucleic Acids Res.*, 1993, 21:3789-3797), and *Candida albicans* (U.S.S.N. ___/____)(Table 1). 2) They contain a predicted DNA-binding region that includes three zinc fingers of the Cys₂His₂ class.

TABLE 1

10	Species of origin	% identity to <i>A. nidulans</i>	% similarity to <i>A. nidulans</i>
	<u>of PacC homolog</u>	<u>PacC in 107-aa</u>	<u>PacC over entire length</u>
	<i>A. Niger</i>	94	75
	<i>P. chrysogenum</i>	84	67
	<i>C. albicans</i>	61	18
15	<i>S. cerevisiae</i>	56	22
	<i>Y. lipolytica</i>	58	30

- In addition, several PacC family member either have been shown to directly bind to or regulate expression of genes that contain a 5'-GCCAAG-3' or 5'-GCCAGG-3' element in upstream regulatory sequence (Tilburn et al., *supra*; Suarez and Penalva, *supra*). Furthermore, with the exception of PacC from *P. chrysogenum*, mutations that truncate the protein have either been identified or constructed, and these mutations result in activation of gene expression by the PacC family of proteins, even at low ambient pH (Tilburn et al., *supra*; van den Hombergh et al., *Mol. Gen. Genet.*, 1996, 251:542-550; Lambert et al., *supra*; Li and Mitchell, *Genetics*, 1997,
- 25 145:63-73). Finally, in both *A. nidulans* and *S. cerevisiae*, it has been demonstrated

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that specific proteolytic cleavage results in activation of signaling *in vivo* (Orejas et al., *Genes Dev.*, 1995, 9:1622-32; Li and Mitchell, *supra*).

Transcription Activation Domains

Transcription activation domains (TADs) are discrete regions of proteins which promote gene expression by a variety of mechanisms that ultimately result in the activation of RNA polymerase. A TAD generally is defined as the minimal motif that activates transcription when fused to a DNA-binding domain (DBD) (Webster et al., *Cell*, 1988, 52:169-178; Fischer et al., *Nature*, 1988, 332:853-856; Hope et al., *Nature*, 1988, 333:635-640). The invention can employ any TAD that can transactivate expression from a fungal gene promoter when the TAD is fused to an appropriate DBD. TADs are classified based on similarities in protein sequence and/or composition properties. These classes include the acidic-rich (e.g., Gal4, Gcn4, VP16, and Jun; Webster et al., *supra*; Fischer et al., *supra*; Hope et al., *supra*; Cress and Triezenberg, *Science*, 1991, 251:87-90; Struhl, *Nature*, 1988, 332:649-650), glutamine-rich (Sp1, Oct1, and Oct2; Courey and Tjian, *Cell*, 1988, 55:887-898; Tanaka et al., *Mol. Cell Biol.*, 1994, 14:6046-6055; Tanaka and Herr, *Mol. Cell Biol.*, 1994, 14:6056-6067), and proline-rich TADs (CTF, NF-I, and EKLF; Mermod et al., *Cell*, 1989, 58:741-753; Tanese et al., *Genes Dev.*, 1991, 5:2212-2224; Chen and Bieker, *EMBO J.*, 1996, 15:5888-5896). Any of these classes of TADs may be used in the present invention. The ability of any particular TAD to transactivate from a particular promoter can be determined using simple, known selection screens.

It is also possible to artificially create either a TAD or a site-specific DBD. In one example, protein sequences which transactivate a reporter gene from a promoter of interest are selected from an expression library. In another example, protein sequences which specifically bind particular DNA sequences are selected. In each case, these sequences can then be mutated in a reiterative process to obtain either the optimal TAD sequence for the particular promoter, or the optimal DBD sequence for a particular DNA sequence. Transcription factors containing artificial elements

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produced by this or any other method are useful in the invention.

- In the chimeric transcription factor of the featured invention, TADs may be used alone or in combination. For example, Sp1 contains multiple glutamine-rich TADs, and these domains act synergistically to promote gene expression (Courey and Tjian, *supra*; Courey et al., *Cell*, 1989, 59:827-836). Oct-2 contains both glutamine-rich and proline-rich TADs, and both are required for maximal expression when fused to either the Oct-2 or a heterologous DBD (Tanaka et al., *supra*). Thus, the use of two or more classes of TADs in one construct may amplify the induction of expression. Furthermore, homopolymeric stretches of proline or glutamine function as TADs (Gerber et al., *Science*, 1994, 263:808-811). In one example, a strong transcription factor has been created by fusion of the Gal4 DBD to a homopolymeric glutamine stretch linked to reiterated VP16 TADs (Schwechheimer et al., *Plant Mol. Biol.*, 1998, 36:195-204).

Fungal Promoters

- The chimeric, pre-activated transcription factor is operably linked to a strong promoter, allowing for expression of the transcription factor in a fungal cell. Expression systems utilizing a wide variety of promoters in many fungi are known, including, but not limited to, *Aspergillus nidulans* (*gpd*: Punt et al., *Gene*, 1987, 56:117-124; Hunter et al., *Curr. Genet.*, 1992, 22:377-383; Glumoff et al., *Gene*, 1989, 84:311-318. *alcA*; Fernandez-Abalos et al., *Mol. Microbiol.*, 1998, 27:121-130. *glaA*: Carrez et al., *Gene*, 1990, 94:147-154. *amdS*: Turnbull et al., *Appl. Environ. Microbiol.*, 1990, 56:2847-2852), *Aspergillus niger* (*gpd*: Punt et al., *supra*; Hunter et al., *supra*; Glumoff et al., *supra*. *glaA*: Tang et al., *Chin. J. Biotechnol.*, 1996, 12:131-136. *amdS* promoter: Turnbull et al., *supra*), *Pichia pastoris* (alcohol oxidase I promoter: Payne et al., *Gene*, 1988, 62:127-134), *Pleurotus ostreatus* (*Lentinus edodes ras* promoter: Yanai et al., *Biosci. Biotechnol. Biochem.*, 1996, 60:472-475), *Phytophthora infestans* (*Bremia lactucae Hsp70*: Judelson et al., *Mol. Plant Microbe Interact.*, 1991, 4:602-607), *Neurospora crassa* (*his3* promoter: Avalos et al., *Curr.*

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- Genet.*, 1989, 16:369-372), *Yarrowia lipolytica* (*XPR2* promoter: Nicaud et al., *Curr. Genet.*, 1989, 16:253-260. *TEF*: Muller et al., *Yeast*, 1998, 14:1267-1283.), *Penicillium chrysogenum* (*phoA* promoter: Graessle et al., *Appl. Environ. Microbiol.*, 1997, 63:753-756), *Rhizopus deleamar* (*pyr4* promoter: Horiuchi et al., *Curr. Genet.*, 1995, 27:472-478), *Gliocladium virens* (*prom1*: Dave et al., *Appl. Microbiol. Biotechnol.*, 1994, 41:352-358), and *Cochliobolus heterostrophus* (Monke and Shafer, *Mol. Gen. Genet.*, 1993, 241:73-80).

There are also simple techniques for isolating promoters in organisms with relatively unstudied genetics. One of these is a system based on selection of sequences with promoter activity (see, for example, Turgeon et al., *Mol. Cell Biol.*, 1987, 7:3297-3305; Weltring, *Curr. Genet.*, 1995, 28:190-196). This approach provides an easy method for isolating promoter fragments from a wide variety of fungi.

The constructs of the invention also preferably include a terminator sequence located 3' to the chimeric transcription factor coding sequence. Terminator sequences which function in numerous fungi are known in the art. These include those from *Aspergillus nidulans trpC* (Punt et al., *supra*; Hunter et al., *supra*; Glumoff et al., *supra*), *Lentinus edodes priA* (Yanai et al., *supra*), *Bremia lactucae Ham34* (Judelson et al., *supra*), and *Aspergillus nidulans argB* (Carrez et al., *supra*).

20 Construction of Chimeric Transcription Factors

The pre-activated transcription factors of the invention display 1) increased binding, either direct or indirect, to a specific DNA sequence located in a gene regulatory region (e.g., a promoter) *in vivo*, and/or 2) increased transcription activating properties, relative to the precursor molecule. To this end, it is preferable that part or all of the DBD, the domain of the parental transcription factor which recognizes and binds to the DNA sequences, remain intact. Additional sequences from the parental transcription factor may also remain in the chimeric construct, or they may be removed. The TAD of the

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parental transcription factor may be removed, as the chimeric transcription factor will contain a TAD from another protein, such as the herpesvirus transactivator VP16, as described herein. The TAD from the parental transcription factor may also remain in the chimeric construct.

5 As described above, TADs can be acidic, glutamine-rich, or proline-rich. The ability of each of these TADs to function in any given fungal strain will vary. The acidic TADs have been shown to function in a wide variety of organisms, from *C. elegans* to humans, including fungi. Glutamine-rich and proline-rich TADs have also been shown to function in disparate organisms,
10 including fungi. As described above, increased transactivation activity may be achieved by using multiple TADs from one category (Tanaka and Herr, *supra*). Furthermore, TADs from more than one class may be used in one chimeric protein (Schwechheimer et al., *supra*; Tanaka et al., *supra*). In the example described below, 4 VP16 TADs and a proline-rich TAD are placed in series.

15 The production of chimeric transcription factors which activate transcription is not limited to the use of parental transcription factors that themselves are transcriptional activators. Using this method, transcription factors which are transcriptional repressors may be converted to transcriptional activators by the addition of a TAD. An example is the *Saccharomyces*
20 *cerevisiae* Mig1, which is a repressor of *SUC2* expression. Deletion of *mig1* derepresses *SUC2* expression. A chimeric protein in which the DBD of Mig1 is fused to the VP16 TAD can activate transcription from promoters containing Mig1-binding sites and leads to increased expression of *SUC2* (Ostling et al., *Mol Cell Biol.*, 1996, 16:753-61). Thus, the formation of a chimeric
25 transcriptional activator may be performed for any transcription factor, whether it be an activator or a repressor.

The choice of parental transcription factor for use in the present

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invention depends upon the desired product one wishes to produce. The transcription factor must recognize a sequence in the promoter of a gene of interest. This gene may encode a protein which itself is a desired product, or one which acts as an element (e.g., an enzyme) in the pathway by which a desired product is made by the host fungal cell. For example, a chimeric transcription factor including PacC may be used if the desire is to increase the production of beta-lactam antibiotics. This is achieved by increasing the expression of at least two genes, *ipnA* and *acvA*, which encode enzymes in the penicillin production process.

One skilled in the art will recognize that there are standard techniques, including the ones described herein, which allow for rapid selection and screening of chimeric transcription factor constructs in order to ascertain which transcription factors are the strongest transcriptional activators.

Construction of Fungal Expression Vectors

To achieve high expression of the chimeric transcription factor, several types of expression vectors are known in the art (e.g., those described herein). The choice of expression vectors may depend on the type of fungus to be used. For example, expression of a chimeric transcription factor in *Aspergillus nidulans* may be achieved using the *amdS* promoter system (Turnbull et al., *supra*). The promoter element may be modified such that it also contains a DNA sequence recognized by the chimeric transcription factor. The expression of the chimeric transcription factor will induce increased activation from its own promoter, thus amplifying its own production. The expression vector may also include terminator sequences, as described above. For example, a suitable terminator for *Aspergillus nidulans* is the *argB* terminator.

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The vector, once transformed into a fungal cell as described herein, may remain episomal, in which case the vector may also have an origin of replication. The vector may also integrate into the chromosomal DNA of the host cell. The expression of the integrated expression construct may depend on positional effects, and, thus, it may be necessary to screen through or select for transformants to isolate those with suitably high expression. Methods for screening and selection are described herein. The integrated expression construct may also alter the expression of endogenous genes of the fungal cell. This altered expression may be beneficial or detrimental to the survival of the cell or to the purpose of the production of the fungal cell. For example, if the purpose is to increase production of a beta-lactam antibiotic, then loss of expression of *ipnA* (which encodes isopenicillin N-synthase and is required for beta-lactam production) following integration of the expression construct would negate any benefits resulting from expression of the chimeric transcription factor. Thus, a secondary screen of transformants displaying characteristics suitably for the designed purpose may be performed. Methods for determining metabolite production are described herein.

In some cases, it may be beneficial to use a transcription factor which is not chimeric. Overexpression of a parental transcription factor may lead to an increase in secondary metabolites. This overexpressed protein may be constitutively active, due to overexpression or genetic mutation, or it may be regulated in a manner similar to the endogenous transcription factor. The fungal cell may be a wild-type strain, or it may contain one or more mutations (which may also increase production of secondary metabolites). Example mutations include those which result in duplication or rearrangement of biosynthetic genes (e.g., the penicillin gene cluster of *ipnA*, *acvA*, and *aatA*). Reporter genes, such as those described herein, or other exogenous genes may

also be present in the fungal cells, either episomally or chromosomally.

Transformation

- In order to introduce the construct into a fungal cell, one may utilize any of numerous transformation protocols (for review, see Punt and van den Hondel, *Methods Enzymol.*, 1992, 216:447-457; Timberlake and Marshall, *Science*, 1989, 244:1313-1317; Fincham, *Microbiol. Rev.*, 1989, 53:148-170). Suitable DNA transformation techniques include electroporation, polyethylene glycol-mediated, lithium acetate-mediated, and biolistic transformation (Brown et al., *Mol. Gen. Genet.*, 1998, 259:327-335; Zapanta et al., *Appl. Environ. Microbiol.*, 1998, 64:2624-2629; Thompson et al., *Yeast*, 1998, 14:565-571; Barreto et al., *FEMS Microbiol. Lett.*, 1997, 156:95-99; Nicolaisen and Geisen, *Microbiol. Res.*, 1996, 151:281-284; Wada et al., *Appl. Microbiol. Biotechnol.*, 1996, 45:652-657; Ozeki et al., *Biosci. Biotechnol. Biochem.*, 1994, 58:2224-2227; Lorito et al., *Curr. Genet.*, 1993, 24:349-356; Oda and Tonomura, *Curr. Genet.*, 1995, 27:131-134). If desired, one may target the DNA construct to a particular locus. Targeting homologous recombination techniques are currently practiced in many fungi, including, but not limited to, *Candida albicans* (Fonzi and Irwin, *Genetics*, 1993, 134: 717-728), *Ustilago maydis* (Fotheringham and Hollman, *Mol. Cell Biol.*, 1989, 9:4052-4055; Bolker et al., *Mol. Gen. Genet.*, 1995, 248:547-552), *Yarrowia lipolytica* (Neueglise et al., *Gene* 1998, 213:37-46; Chen et al., *Appl. Microbiol. Biotechnol.*, 1997, 48:232-235; Cordero et al., *Appl. Microbiol. Biotechnol.*, 1996, 46:143-148), *Acremonium chrysogenum* (Skatrud et al., *Curr. Genet.*, 1987, 12:337-348; Walz and Kuck, *Curr. Genet.*, 1993, 24:421-427), *Magnaporthe grisea* (Sweigard et al., *Mol. Gen. Genet.*, 1992, 232:183-190); Kershaw et al., *EMBO J.*, 1998, 17:3838-3849), *Histoplasma capsulatum* (Woods et al., *J. Bacteriol.*, 1998, 180:5135-5143)

and *Aspergillus* sp. (Miller et al., *Mol. Cell Biol.*, 1985, 5:1714-1721; de Ruiter-Jacobs et al., *Curr. Genet.*, 1989, 16:159-163; Gouka et al., *Curr. Genet.*, 1995, 27:536-540; van den Hombergh et al., *Mol. Gen. Genet.*, 1996, 251:542-550; D'Enfert, *Curr. Genet.*, 1996, 30:76-82; Weidner et al., *Curr. Genet.*, 1998, 33:378-385).

Methods for Selection and Screening Transformants

Reporter genes are useful for isolating transformants expressing functional chimeric transcription factors. The reporter genes may be operably linked to promoter sequence which is regulated by the chimeric transcription factor. Reporter genes include, but are not limited to, genes encoding β -galactosidase (*lacZ*), β -glucuronidase (*GUS*), β -glucosidase, and invertase, amino acid biosynthetic genes, e.g., the yeast *LEU2*, *HIS3*, *LYS2*, *TRP1* genes (or homologous genes from other fungi, such as filamentous fungi, that encode proteins with the similar functional activities), nucleic acid biosynthetic genes, e.g., the yeast *URA3* and *ADE2* genes (or homologous genes from other fungi, such as filamentous fungi, that encode proteins with the similar functional activities), the mammalian chloramphenicol transacetylase (*CAT*) gene, or any surface antigen gene for which specific antibodies are available. A reporter gene may encode a protein detectable by luminescence or fluorescence, such as green fluorescent protein (*GFP*). Reporter genes may encode also any protein that provides a phenotypic marker, for example, a protein that is necessary for cell growth or viability, or a toxic protein leading to cell death, or the reporter gene may encode a protein detectable by a color assay leading to the presence or absence of color.

The choice of reporter gene will depend on the type of fungal cell to be transformed. It is preferable to have two reporter genes within the fungal

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cell. One reporter gene, when expressed, may provide a growth advantage to transformed cells which are expressing the chimeric transcription factor. This allows for isolation of such transformants though selective pressures. The other reporter gene may provide a colorimetric marker, such as the *lacZ* gene and its encoded protein, β -galactosidase. Alternatively, the second reporter may provide a fluorescent or luminescent marker, such as GFP. These reporters provide a method of quantifying expression levels from expression constructs comprising chimeric transcription factors. Screens and selections similar to the ones described may be used to optimize construction of chimeric transcription factors or expression constructs.

Example

The following example describes a method for increasing the level of PacC activity over that caused by proteolysis or specific truncations. This invention may facilitate the increased production of fungal secondary metabolites including, but not limited to, penicillins and cephalosporins. Similar genetic engineering can be performed to alter the function of other transcription factors.

A construct that encodes a chimeric transcription factor is described below. In this example, a proline-rich TAD followed by multiple copies of the acidic-rich TAD from the herpes simplex virus VP16 protein are fused to a truncated, pre-activated PacC from *Aspergillus nidulans* (SEQ ID NO: 7). This construct may be integrated at the *pyrG* locus in *Aspergillus nidulans*, as described below. Expression of this chimeric polypeptide is regulated by the strong PGK promoter from *Aspergillus nidulans* and terminator sequences from the *crnA* gene of *Aspergillus nidulans*.

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- Several DNA cloning steps are required to create this chimeric construct. Bluescript KS (Stratagene, LaJolla, CA) is used as a cloning vector. The primers 5'-aactgcagTAGTTGACCGTGTGATTGGGTTCT-3' (SEQ ID NO: 8) (lowercase letters denote sequences introduced for cloning and restriction sites are underlined) and 5'-ccggaattcTTTGTAAACTGGCTTGAAGAT-3' (SEQ ID NO: 9) are used to amplify 347bp of *crnA* terminator sequence from genomic DNA template. The PCR product is *Pst*I/*Eco*RI digested and then cloned into the KS polylinker to produce p1. Subsequently, complementary oligonucleotides 5'-gatccCCCCCCCCCTCCTCCACCCCCACCCCTCCC-3' (SEQ ID NO: 10) and 5'-GGGAGGGGGTGGGGGTGGAGGAGGGGGGGGg-3' (SEQ ID NO: 11) are annealed (this double-stranded oligonucleotide encodes a proline-rich motif) and the double-stranded product is ligated into *Sma*I/*Bam*HI digested p1, yielding p2.
- Next, the oligonucleotide primers 5'-cgcgatacAAAGTCGCCCCCGACCGAT-3' (SEQ ID NO: 12) and 5'-cgcgatacCCCACCGTACTCGTCAATTCC-3' (SEQ ID NO: 13) are used in PCR reactions to amplify a 258bp fragment using pVP16 (Clontech, Palo Alto, CA) as template. This product encodes the acidic-rich domain of VP16. The product is digested with *Eco*RV, and ligation reaction is performed with >20 fold excess of *Eco*RV insert relative to *Sma*I-digested calf-alkaline phosphatase treated p2. Bacterial transformants are screened for plasmids that contain multiple tandem insertions of VP16 sequence. *Sma*I sites within the VP16 coding sequence allow for determination of the orientation of the insertion.
- Plasmids are selected that contain four insertions of the VP16 acidic-rich domain (p3). p3, then, encodes a proline-rich domain in-frame with four

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reiterations of the VP16 domain, and these TADs are linked to the *crnA* terminator.

In the next cloning step a truncated form of *pacC* is fused to the coding sequence for the TADs. Primers 5'-

- 5' tgctctagaGGCGCCATGGCCGAAGAAGCG -3' (SEQ ID NO: 14) and 5'-
cgcggaatccGTAACCAGAAGTCATACCGTC -3' (SEQ ID NO: 15) are used to
amplify a 1419bp product (SEQ ID NO: 16) from an *Aspergillus nidulans*
cDNA library. This product is *XbaI/BamHI* digested and ligated into digested
p3 to produce p4. This cloning reaction introduces a form of *pacC* that lacks
10 the carboxy-terminal 209 amino acids in-frame with the described TADs.

- An additional cloning step is required in order to place the coding
sequence for this chimera under the control of a strong promoter. Primers 5'-
ataagaatgcggcgcCCTCTGCATTATTGTCTTATC -3' (SEQ ID NO: 17) and
5'- tgctctagaAGACATTGTTGCTATAGCTGT -3' (SEQ ID NO: 18) are used
15 to amplify 689bp of PGK promoter sequence (SEQ ID NO: 19) from
Aspergillus nidulans genomic DNA. This fragment is *NotI/XbaI* digested and
cloned into digested p4 in order to yield p5. Thus, p5 contains coding sequence
for an 815 amino acid chimeric transcription factor to be expressed from the
PGK promoter.

- 20 To decrease the extent of position effects, the p5 construct is targeted
to the *pyrG* locus. Oligonucleotides 5'-

- tcccgcggATGGAAGCTTCGTTAAGGATAATT-3' (SEQ ID NO: 20) and 5'-
ataagaatgcggcgcCTACCAGATTAGGGAGCATAT-3' (SEQ ID NO: 21) are
used to amplify a 2240bp product (SEQ ID NO: 22) from *Aspergillus nidulans*
25 genomic DNA; this product contains coding and regulatory sequence for the
pyrG gene that encodes orotidine-5'- phosphate decarboxylase. The 2240bp
fragment is *SacII/NotI* digested, and then cloned into p5 to produce p6; this

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fragment is also cloned into KS to yield p7 (a control construct, containing regulatory sequence for the *pyrG* gene, but no PGK promoter or transcription factor). p6 and p7 are vector that can complement uridine auxotrophy, allowing for selection, and target the chimeric transcription factor to the *pyrG* locus. In addition, primers 5'- tgctctagaGGCGCCATGGCCGAAGAAGCG -3' (SEQ ID NO: 23) and 5' tccccgggGTAACCAGAAGTCATACCGTC -3' (SEQ ID NO: 24) are used to amplify the truncated form of PacC from an *Aspergillus nidulans* cDNA library. This fragment can be cloned into *XbaI/SmaI* digested p6 to produce p8. p8 is a control construct, used to monitor the activity of pre-activated PacC expressed from the PGK promoter, independent of the presence of heterologous TADs.

PEG- CaCl_2 (or other methods, described herein) may be used to transform protoplasts of a uridine auxotroph carrying a *pyrG* mutation (Ballance and Turner, *Gene*, 1985, 36:321-331). p6, p7, and p8 plasmid DNA are used to transform to uridine prototrophy. PCR and Southern analysis are performed to confirm single-copy integration at *pyrG*.

Several methods may be employed to assess the activity of wild-type, pre-activated, and chimeric PacC-TAD factors. Samples of mycelia may be taken from parallel fermentation of strains containing p6, p7, and p8. Northern blot analysis may be performed on RNA prepared from extracts of these mycelia. Probes are prepared from coding sequence for the *ipnA* and *acvA* genes of *Aspergillus nidulans*. Reporter constructs are valuable tools for examining the level of PacC activation. For example, *ipnA* and *acvA* are divergently transcribed from a common regulatory sequence. One may use constructs (e.g., pAXB4A; Brakhage et al., *supra*) that contain *ipnA-lacZ* and *acvA-uidA* reporters within the same plasmid; this particular plasmid can be targeted to the *argB* locus to ensure integration at a specific genomic locus. A

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strain carrying both *argB* and *pyrG* mutations can be sequentially transformed with the *pyrG* and reporter vectors, and enzyme assays can be performed on extracts from mycelia (van Gorcom et al., *Gene*, 1985, 40:99-106; Pobjecky et al., *Mol. Gen. Genet.*, 1990, 220:314-316). In addition, bioassays can be done to determine whether chimeric transcription factors increase the production of fungal secondary metabolites such as penicillin. Supernatant fluid from fermentations can be centrifuged and applied to wells containing indicator organisms such as *Bacillus calidolactis* (Smith et al., *Mol. Gen. Genet.*, 1989, 216:492-497). The application of all of these methods will promote a rapid and quantitative analysis of the efficacy of chimeric transcription factors.

Enhancement of Secondary Metabolite Production

The constructs and methods described herein may be used to increase the yields of currently marketed pharmaceuticals whose production, in whole or in part, is dependent upon a fungal fermentation. For example, in *Aspergillus nidulans*, penicillin biosynthesis is catalyzed by three enzymes encoded by *ipnA*, *acvA*, and *aatA*. Two of these genes, *ipnA* and *acvA*, are regulated directly by PacC. For example, *P_{ipnA}* contains at least three PacC binding sites (*ipnA2*, *ipnA3*, and *ipnA4AB*) (Espeso and Penalva, *J. Biol. Chem.*, 1996, 271:28825-28830). Expression of a truncated form of PacC has been shown to increase both expression of *ipnA* and *acvA* as well as production of penicillin. Activation (i.e., proteolytic cleavage) of PacC requires the proteins encoded by the *palA*, *palB*, *palC*, *palF*, *palH*, and *palI* genes. It is possible that increased expression of at least some of these genes would result in increased production of penicillin. In the example described herein, *ipnA* and *acvA* expression are targeted for increase by formation of a chimeric transcription factor including the DNA-binding domain of PacC and 4 VP16 acidic TADs and a proline-rich

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TAD. Using the methods of the invention, production of other secondary metabolites can also be increased.

Examples of marketed secondary metabolites whose yields during fermentation could be increased by the methods of the invention include, without limitation, cyclosporin, penicillin, cephalosporin, ergot alkaloids, lovastatin, mevastatin, and the biosynthetic intermediates thereof. In addition, such methods can also be used to increase the likelihood of identifying new secondary metabolites with medicinal or agricultural value by increasing the concentration of such metabolites (and hence, the likelihood of detection by chemical or bioassay) in a fermentation broth.

Production and Detection Methods for Fungal Secondary Metabolites

Methods for fermentation and production of beta-lactam antibiotics, statins, ergot alkaloids, cyclosporin, and other fungal metabolites are described in Masurekar (*Biotechnology*, 1992, 21: 241-301), and references therein. The detection of secondary metabolites is specific for each metabolite and well-known to those practiced in the art. General methods to assess production and integrity of compounds in fermentation broths include, but are not limited to, bioassays for antimicrobial activity, high-performance liquid chromatography (HPLC) analysis, nuclear magnetic resonance, thin-layer chromatography, and absorbance spectrometry. Purification of metabolites from a fermentation broth can include removal of fungal cells or hyphae by centrifugation or filtration, adjustment of pH and/or salt concentrations after fermentation (to enhance solubility and/or subsequent extraction efficiency), and extraction of broths with appropriate organic solvents.

What is claimed is:

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1. A chimeric transcription factor comprising
 - (a) a pre-activated transcription factor functional in a fungal strain,
and
 - (b) a transcription activation domain that is different from the
5 transcription activation domain naturally associated with said transcription
factor.
2. The chimeric transcription factor of claim 1, wherein said
chimeric transcription factor activates transcription in a manner greater than
said pre-activated transcription factor.
- 10 3. The chimeric transcription factor of claim 1, wherein said pre-
activated transcription factor is pre-activated by truncation.
4. The chimeric transcription factor of claim 1, wherein said pre-
activated transcription factor comprises a substitution of a serine or threonine
residue with an alanine, aspartic acid, or glutamic acid residue, wherein said
15 substitution pre-activates said transcription factor.
5. The chimeric transcription factor of claim 3, wherein said pre-
activated transcription factor is substantially identical to *Aspergillus nidulans*
PacC.
6. A chimeric transcription factor comprising
 - (a) a transcription factor substantially identical to *Aspergillus*
20 *nidulans* PacC, and

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(b) a transcription activation domain that is different from the transcription activation domain naturally associated with said transcription factor.

7. The chimeric transcription factor of claim 1, wherein said pre-activated transcription factor comprises amino acid sequence shown in Fig. 1 (SEQ ID Nos: 1-6).

8. The chimeric transcription factor of claim 1, wherein said pre-activated transcription factor binds to a DNA sequence comprising 5'-GCCAAG-3' or 5'-GCCAGG-3'.

10 9. A vector comprising DNA encoding the chimeric transcription factor of claim 1 operably linked to a promoter capable of controlling expression of said chimeric transcription factor in a fungal strain.

10. A fungal cell that contains and expresses the DNA of claim 9.

15 11. The fungal cell of claim 10, wherein said fungal cell is a filamentous fungal cell.

12. The fungal cell of claim 10, wherein said cell produces a secondary metabolite and wherein expression of said DNA increases the production of said secondary metabolite by said cell.

20 13. The fungal cell of claim 12, wherein said secondary metabolite is non-proteinaceous.

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14. The fungal cell of claim 12, wherein said secondary metabolite is a protein or peptide.

15. A method of producing a secondary metabolite, said method comprising culturing the fungal cell of claim 10 under secondary metabolite-producing conditions.

16. A method of producing a secondary metabolite, said method comprising the steps of

(a) introducing into a fungal cell a vector comprising (i) a promoter capable of controlling gene expression in said fungal cell, and (ii) a nucleic acid encoding a transcription factor comprising (i) a DNA-binding domain and (ii) a transcription activation domain; and

(b) culturing said fungal cell under secondary metabolite-producing conditions.

17. The method of claim 16, wherein said fungal cell is a filamentous fungal cell.

18. The method of claim 16, wherein said transcription factor is a chimeric transcription factor.

19. The method of claim 16, wherein said transcription factor is a pre-activated transcription factor.

20. The method of claim 16, wherein said transcription factor is pre-activated by substitution of a serine or threonine residue with an alanine,

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aspartic acid, or glutamic acid residue, wherein said substitution pre-activates said transcription factor.

21. The method of claim 16, wherein said transcription factor is pre-activated by truncation.

5 22. The method of claim 16, wherein said DNA binding domain is from a fungal transcriptional activator.

23. The method of claim 16, wherein said DNA binding domain is from a fungal transcriptional repressor.

10 24. The method of claim 16, wherein said transcription activation domain that is different from the transcription activation domain naturally associated with said transcription factor.

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141	A. nidulans	141	QNL	SLP	VT	TA	PL	PE	YO	AM	PA	VA	VA	..	GG	PY	..	GG	PA	PA	YH	LP	PM	SN	VR	AT	KN	..	DL	IN							
142	A. niger	142	OS	SL	PL	VT	SS	GP	LE	YO	AM	PA	VA	VA	..	GG	PY	..	GG	PA	PA	YH	LP	PM	SN	VR	AT	KN	..	DL	IN						
143	P. doyngium	143	QAL	SL	PL	VT	SS	GP	LE	YO	AM	PA	VA	VA	..	GG	PY	..	GG	PA	PA	YH	LP	PM	SN	VR	AT	KN	..	DL	IN						
144	P. horikae	144	EQ	YI	GL	TO	GO	OO	Q	Q	SS	PT	PI	AT	IT	SA	TA	PA	PA	PH	AT	PO	LO	PS	FX	GO	LD	VE					
145	C. albicans	145	K	RM	KA	ST	EL	YV	NI	LO	FI	AN	KL	HL	DO	HL	EH	HP	QO	GH	..	QO	YV	GN	..	LY	VE						
146	S. cerevisiae	146	NS	RS	MN	YV	DE	OG	CS	NK	IT	AN	KL	SR	NA	NN	VI	LO	Q	SS	GT	ES	SS	SG	..	PI	VA						
147	A. nidulans	147	LDQ	FL	QO	OD	TI	VE	ND	DA	VA	AA	GV	AA	Q	PA	HY	..	NG	SY	AT	TH	SP	AT	Q	LP	SA	HA	TT	OT	TA						
148	A. niger	148	IDQ	FL	QO	OD	TI	VE	ND	DA	VA	AA	GV	AA	Q	PA	HY	..	NG	SY	AT	TH	SP	AT	Q	LP	SA	HA	TT	OT	TA						
149	P. doyngium	149	LDQ	FL	QO	OD	TI	VE	ND	DA	VA	AA	GV	AA	Q	PA	HY	..	NG	SY	AT	TH	SP	AT	Q	LP	SA	HA	TT	OT	TA						
150	P. horikae	150	AE	RF	FN	LS	NI	YV	GN	IT	YV	GN	IT	YV	GN	IT	YV	..	GM	NN	HT	TH	SP	AT	Q	LP	SA	HA	TT	OT	TA						
151	C. albicans	151	OT	SY	VB	OB	PN	AB	SV	SO	SV	GO	SS	IT	SA	TA	..	NT	AT	YV	VP	VR	AK	YV	IT	GP	RS	IT						
152	S. cerevisiae	152	GP	IT	SN	TS	AH	SS	PS	ST	PA	LT	PP	SS	AA	Q	SY	TS	GR	SP	IS	..	PS	AT	RV	SS	PR	HE	GG	..	SM	VP	TR	PS	SA		
153	A. nidulans	153	P	..	MA	PA	TA	HS	PS	VG	IT	PA	LT	PP	SS	AA	Q	SY	TS	GR	SP	IS	..	PS	AT	RV	SS	PR	HE	GG	..	SM	VP	TR	PS	SA	
154	P. doyngium	154	AP	..	HQ	AP	..	VA	HO	VA	AP		
155	P. horikae	155			
156	C. albicans	156			
157	S. cerevisiae	157			
158	A. nidulans	158	T	..	OG	MT	SG	YV	TA	AS	SA	AP	PS	TT	GG	..	FE	ND	DA	VA	AA	GV	AA	Q	PA	HY	..	NG	SY	AT	TH	SP	AT	Q	LP	SA	
159	A. niger	159	IT	MA	OS	MA	AG	YV	TA	AS	SA	AP	PS	TT	GG	..	FE	ND	DA	VA	AA	GV	AA	Q	PA	HY	..	NG	SY	AT	TH	SP	AT	Q	LP	SA	
160	P. doyngium	160	R	IT	CA	DS	MT	AG	YV	TA	AS	SA	AP	PS	TT	GG	..	FE	ND	DA	VA	AA	GV	AA	Q	PA	HY	..	NG	SY	AT	TH	SP	AT	Q	LP	SA
161	P. horikae	161	N		
162	C. albicans	162	G		
163	S. cerevisiae	163		
164	A. nidulans	164	ES	GE	RT	PK	Q	IS	AS	SL	DP	AL	HS	GS	..	PG	EO	DT	RT	PK	
165	A. niger	165	DE	GE	RT	PK		
166	P. doyngium	166	HD	GE	RT	PK		
167	P. horikae	167		
168	C. albicans	168		
169	S. cerevisiae	169		
170	A. nidulans	170	WE	VE	K	AT	LL	LE	Y	LN	Y	A	SL	LE	GE	FE	SD	..	SE	QO	DO	QO	QO	DO	QO	QO	DO	QO	QO	DO	QO	QO	DO	QO	QO	DO	
171	A. niger	171	WE	VE	K	AT	LL	LE	Y	LN	Y	A	SL	LE	GE	FE	SD	..	SE	QO	DO	QO	QO	DO	QO	QO	DO	QO	QO	DO	QO	QO	DO	QO	QO	DO	
172	P. doyngium	172	WE	VE	K	AT	LL	LE	Y	LN	Y	A	SL	LE	GE	FE	SD	..	SE	QO	DO	QO	QO	DO	QO	QO	DO	QO	QO	DO	QO	QO	DO	QO	QO	DO	
173	P. horikae	173	WE	VE	K	AT	LL	LE	Y	LN	Y	A	SL	LE	GE	FE	SD	..	SE	QO	DO	QO	QO	DO	QO	QO	DO	QO	QO	DO	QO	QO	DO	QO	QO	DO	
174	C. albicans	174	WE	VE	K	AT	LL	LE	Y	LN	Y	A	SL	LE	GE	FE	SD	..	SE	QO	DO	QO	QO	DO	QO	QO	DO	QO	QO	DO	QO	QO	DO	QO	QO	DO	
175	S. cerevisiae	175	WE	VE	K	AT	LL	LE	Y	LN	Y	A	SL	LE	GE	FE	SD	..	SE	QO	DO	QO	QO	DO	QO	QO	DO	QO	QO	DO	QO	QO	DO	QO	QO	DO	
176	A. nidulans	176	WE	VE	K	AT	LL	LE	Y	LN	Y	A	SL	LE	GE	FE	SD	..	SE	QO	DO	QO	QO	DO	QO	QO	DO	QO	QO	DO	QO	QO	DO	QO	QO	DO	
177	A. niger	177	WE	VE	K	AT	LL	LE	Y	LN	Y	A	SL	LE	GE	FE	SD	..	SE	QO	DO	QO	QO	DO	QO	QO	DO	QO	QO	DO	QO	QO	DO	QO	QO	DO	
178	P. doyngium	178	WE	VE	K	AT	LL	LE	Y	LN	Y	A	SL	LE	GE	FE	SD	..	SE	QO	DO	QO	QO	DO	QO	QO	DO	QO	QO	DO	QO	QO	DO	QO	QO	DO	
179	P. horikae	179	WE	VE	K	AT	LL	LE	Y	LN	Y	A	SL	LE	GE	FE	SD	..	SE	QO	DO	QO	QO	DO	QO	QO	DO	QO	QO	DO	QO	QO	DO	QO	QO	DO	
180	C. albicans	180	WE	VE	K	AT	LL	LE	Y	LN	Y	A	SL	LE	GE	FE	SD	..	SE	QO	DO	QO	QO	DO	QO	QO	DO	QO	QO	DO	QO	QO	DO	QO	QO	DO	
181	S. cerevisiae	181	WE	VE	K	AT	LL	LE	Y	LN	Y	A	SL	LE	GE	FE	SD	..	SE	QO	DO	QO	QO	DO	QO	QO	DO	QO	QO	DO	QO	QO	DO	QO	QO	DO	
182	A. nidulans	182	OT	YV	OB	PN	AB	SV	SO	SV	GO	SS	IT	SA	TA	..	NT	AT	YV	VP	VR	AK	YV	IT	GP	RS	IT		
183	A. niger	183	OT	YV	OB	PN	AB	SV	SO	SV	GO	SS	IT	SA	TA	..	NT	AT	YV	VP	VR	AK	YV	IT	GP	RS	IT		
184	P. doyngium	184	OT	YV	OB	PN	AB	SV	SO	SV	GO	SS	IT	SA	TA	..	NT	AT	YV	VP	VR	AK	YV	IT	GP	RS	IT		
185	P. horikae	185	OT	YV	OB	PN	AB	SV	SO	SV	GO	SS	IT	SA	TA	..	NT	AT	YV	VP	VR	AK	YV	IT	GP	RS	IT		
186	C. albicans	186	OT	YV	OB	PN	AB	SV	SO	SV	GO	SS	IT	SA	TA	..	NT	AT	YV	VP	VR	AK	YV	IT	GP	RS	IT		
187	S. cerevisiae	187	OT	YV	OB	PN	AB	SV	SO	SV	GO	SS	IT	SA	TA	..	NT	AT	YV	VP	VR	AK	YV	IT	GP	RS	IT		
188	A. nidulans	188	OT	YV	OB	PN	AB	SV	SO	SV	GO	SS	IT	SA	TA	..	NT	AT	YV	VP	VR	AK	YV	IT	GP	RS	IT		
189	A. niger	189	OT	YV	OB	PN	AB	SV	SO	SV	GO	SS	IT	SA	TA	..	NT	AT	YV	VP	VR	AK	YV	IT	GP	RS	IT		
190	P. doyngium	190	OT	YV	OB	PN	AB	SV	SO	SV	GO	SS	IT	SA	TA	..	NT	AT	YV	VP	VR	AK	YV	IT	GP	RS	IT		
191	P. horikae	191	OT	YV	OB	PN	AB	SV	SO	SV	GO	SS	IT	SA	TA	..	NT	AT	YV	VP	VR	AK	YV	IT	GP	RS	IT		
192	C. albicans	192	OT	YV	OB	PN	AB	SV	SO	SV	GO	SS	IT	SA	TA	..	NT	AT	YV	VP	VR	AK	YV	IT	GP	RS	IT		
193	S. cerevisiae	193	OT	YV	OB	PN	AB	SV	SO	SV	GO	SS	IT	SA	TA	..	NT	AT	YV	VP	VR	AK	YV	IT	GP	RS	IT		
194	A. nidulans	194	OT	YV	OB	PN	AB	SV	SO	SV	GO	SS	IT	SA	TA	..	NT																				

SEQUENCE LISTING

<110> Microbia, Inc.

<120> CHIMERIC PRE-ACTIVATED TRANSCRIPTION
FACTORS

<130> 50078/004WO2

<150> 60/066,129

<151> 1997-11-19

<150> 60/066,308

<151> 1997-11-21

<150> 60/066,462

<151> 1997-11-24

<160> 24

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 678

<212> PRT

<213> *Aspergillus nidulans*

<400> 1

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Thr Val Thr Ser Pro Ser Val Thr Ala Thr Ala Ala Ala Thr Ala
          35          40          45
Ala Val Ala Ser Pro Gln Ala Asn Gly Asn Ala Ala Ser Pro Val Ala
 50          55          60
Pro Ala Ser Ser Thr Ser Arg Pro Ala Glu Glu Leu Thr Cys Met Trp
 65          70          75          80
Gln Gly Cys Ser Glu Lys Leu Pro Thr Pro Glu Ser Leu Tyr Glu His
          85          90          95
Val Cys Glu Arg His Val Gly Arg Lys Ser Thr Asn Asn Leu Asn Leu
100          105          110
Thr Cys Gln Trp Gly Ser Cys Arg Thr Thr Thr Val Lys Arg Asp His
115          120          125
Ile Thr Ser His Ile Arg Val His Val Pro Leu Lys Pro His Lys Cys
130          135          140
Asp Phe Cys Gly Lys Ala Phe Lys Arg Pro Gln Asp Leu Lys Lys His
145          150          155          160
Val Lys Thr His Ala Asp Asp Ser Val Leu Val Arg Ser Pro Glu Pro
          165          170          175
Gly Ser Arg Asn Pro Asp Met Met Phe Gly Gly Asn Gly Lys Gly Tyr
180          185          190
Ala Ala Ala His Tyr Phe Glu Pro Ala Leu Asn Pro Val Pro Ser Gln
195          200          205

```


Gly Tyr Ala His Gly Pro Pro Gln Tyr Tyr Gln Ala His His Ala Pro
 210 215 220
 Gln Pro Ser Asn Pro Ser Tyr Gly Asn Val Tyr Tyr Ala Leu Asn Thr
 225 230 235 240
 Gly Pro Glu Pro His Gln Ala Ser Tyr Glu Ser Lys Lys Arg Gly Tyr
 245 250 255
 Asp Ala Leu Asn Glu Phe Phe Gly Asp Leu Lys Arg Arg Gln Phe Asp
 260 265 270
 Pro Asn Ser Tyr Ala Ala Val Gly Gln Arg Leu Leu Ser Leu Gln Asn
 275 280 285
 Leu Ser Leu Pro Val Leu Thr Ala Ala Pro Leu Pro Glu Tyr Gln Ala
 290 295 300
 Met Pro Ala Pro Val Ala Val Ala Ser Gly Pro Tyr Gly Gly Gly Pro
 305 310 315 320
 His Pro Ala Pro Ala Tyr His Leu Pro Pro Met Ser Asn Val Arg Thr
 325 330 335
 Lys Asn Asp Leu Ile Asn Ile Asp Gln Phe Leu Gln Gln Met Gln Asp
 340 345 350
 Thr Ile Tyr Glu Asn Asp Asp Asn Val Ala Ala Gly Val Ala Gln
 355 360 365
 Pro Gly Ala His Tyr Ile His Asn Gly Ile Ser Tyr Arg Thr Thr His
 370 375 380
 Ser Pro Pro Thr Gln Leu Pro Ser Ala His Ala Thr Thr Gln Thr Thr
 385 390 395 400
 Ala Gly Pro Ile Ile Ser Asn Thr Ser Ala His Ser Pro Ser Ser Ser
 405 410 415
 Thr Pro Ala Leu Thr Pro Pro Ser Ser Ala Gln Ser Tyr Thr Ser Gly
 420 425 430
 Arg Ser Pro Ile Ser Leu Pro Ser Ala His Arg Val Ser Pro Pro His
 435 440 445
 Glu Ser Gly Ser Ser Met Tyr Pro Arg Leu Pro Ser Ala Thr Asp Gly
 450 455 460
 Met Thr Ser Gly Tyr Thr Ala Ala Ser Ser Ala Ala Pro Pro Ser Thr
 465 470 475 480
 Leu Gly Gly Ile Phe Asp Asn Asp Glu Arg Arg Tyr Thr Gly Gly
 485 490 495
 Thr Leu Gln Arg Ala Arg Pro Ala Ser Arg Ala Ala Ser Glu Ser Met
 500 505 510
 Asp Leu Ser Ser Asp Asp Lys Glu Ser Gly Glu Arg Thr Pro Lys Gln
 515 520 525
 Ile Ser Ala Ser Leu Ile Asp Pro Ala Leu His Ser Gly Ser Pro Gly
 530 535 540
 Glu Asp Asp Val Thr Arg Thr Ala Lys Ala Ala Thr Glu Val Ala Glu
 545 550 555 560
 Arg Ser Asp Val Gln Ser Glu Trp Val Glu Lys Val Arg Leu Ile Glu
 565 570 575
 Tyr Leu Arg Asn Tyr Ile Ala Asn Arg Leu Glu Arg Gly Glu Phe Ser
 580 585 590
 Asp Asp Ser Glu Gln Glu Gln Asp Gln Glu Gln Glu Gln Asp Gln Glu
 595 600 605
 Gln Glu Gln Asp Gln Glu Gln Gly Gln Asp Arg Val Ser Arg Ser Pro
 610 615 620
 Val Ser Lys Ala Asp Val Asp Met Glu Gly Val Glu Arg Asp Ser Leu
 625 630 635 640
 Pro Arg Ser Pro Arg Thr Val Pro Ile Lys Thr Asp Gly Glu Ser Ala

645
 Glu Asp Ser Val Met Tyr Pro Thr Leu Arg Gly Leu Asp Glu Asp Gly
 660
 Asp Ser Lys Met Pro Ser
 675

<210> 2
 <211> 667
 <212> PRT
 <213> Aspergillus niger

<400> 2
 Met Ser Glu Pro Gln Asp Thr Thr Thr Ala Pro Ser Thr Thr Ala Ala
 1 5 10 15
 Pro Met Pro Thr Ser Thr Ser Gln Asp Ser Pro Ser Ala Gln Gln Pro
 20 25 30
 Ala Gln Val Ser Ser Ala Thr Ala Ala Ser Ala Ala Thr Ala Ala
 35 40 45
 Ala Ala Ser Ala Ala Val Ala Asn Pro Pro Met Asn Gly Thr Thr Thr
 50 55 60
 Arg Pro Ser Glu Glu Leu Ser Cys Leu Trp Gln Gly Cys Ser Glu Lys
 65 70 75 80
 Cys Pro Ser Pro Glu Ala Leu Tyr Glu His Val Cys Glu Arg His Val
 85 90 95
 Gly Arg Lys Ser Thr Asn Asn Leu Asn Leu Thr Cys Gln Trp Gly Ser
 100 105 110
 Cys Arg Thr Thr Thr Val Lys Arg Asp His Ile Thr Ser His Ile Arg
 115 120 125
 Val His Val Pro Leu Lys Pro His Lys Cys Asp Phe Cys Gly Lys Ala
 130 135 140
 Phe Lys Arg Pro Gln Asp Leu Lys Lys His Val Lys Thr His Ala Asp
 145 150 155 160
 Asp Ser Val Leu Val Arg Ser Pro Glu Pro Gly Ala Arg Asn Pro Asp
 165 170 175
 Met Met Phe Gly Gly Gly Ala Lys Gly Tyr Ala Thr Ala Ala His Tyr
 180 185 190
 Phe Glu Pro Ala Leu Asn Ala Val Pro Ser Gln Gly Tyr Ala His Gly
 195 200 205
 Ala Pro Gln Tyr Tyr Gln Ser His Pro Pro Pro Gln Pro Ala Asn Pro
 210 215 220
 Ser Tyr Gly Asn Val Tyr Tyr Ala Leu Asn His Gly Pro Glu Ala Gly
 225 230 235 240
 His Ala Ser Tyr Glu Ser Lys Lys Arg Gly Tyr Asp Ala Leu Asn Glu
 245 250 255
 Phe Phe Gly Asp Leu Lys Arg Arg Gln Phe Asp Pro Asn Ser Tyr Ala
 260 265 270
 Ala Val Gly Gln Arg Leu Leu Gly Leu Gln Ser Leu Ser Leu Pro Val
 275 280 285
 Leu Ser Ser Gly Pro Leu Pro Glu Tyr Gln Pro Met Pro Ala Pro Val
 290 295 300
 Ala Val Gly Gly Gly Gly Tyr Ser Pro Gly Gly Ala Pro Ser Ala Pro
 305 310 315 320
 Ala Tyr His Leu Pro Pro Met Ser Asn Val Arg Thr Lys Asn Asp Leu
 325 330 335
 Ile Asn Ile Asp Gln Phe Leu Gln Gln Met Gln Asp Thr Ile Tyr Glu

```

          340          345          350
Asn Asp Asp Asn Val Ala Ala Ala Gly Val Ala Gln Pro Gly Ala His
          355          360          365
Tyr Val His Gly Gly Met Ser Tyr Arg Thr Thr His Ser Pro Pro Thr
          370          375          380
Gln Leu Pro Pro Ser His Ala Thr Ala Thr Ser Ser Ala Ser Met Met
          385          390          395
Pro Asn Pro Ala Thr His Ser Pro Ser Thr Gly Thr Pro Ala Leu Thr
          405          410          415
Pro Pro Ser Ser Ala Gln Ser Tyr Thr Ser Gly Arg Ser Pro Val Ser
          420          425          430
Leu Pro Ser Ala Thr Arg Val Ser Pro Pro His His Glu Gly Gly Ser
          435          440          445
Met Tyr Pro Arg Leu Pro Ser Ala Thr Met Ala Asp Ser Met Ala Ala
          450          455          460
Gly Tyr Pro Thr Ala Ser Ser Thr Ala Pro Pro Ser Thr Leu Gly Gly
          465          470          475
Ile Phe Asp His Asp Asp Arg Arg Arg Tyr Thr Gly Gly Thr Leu Gln
          485          490          495
Arg Ala Arg Pro Glu Thr Arg Gln Leu Ser Glu Glu Met Asp Leu Thr
          500          505          510
Gln Asp Ser Lys Asp Glu Gly Glu Arg Thr Pro Lys Ala Lys Glu His
          515          520          525
Ser Ser Pro Ser Ser Pro Glu Arg Ile Ser Ala Ser Leu Ile Asp Pro
          530          535          540
Ala Leu Ser Gly Thr Ala Ala Glu Ala Glu Thr Leu Arg Thr Ala
          545          550          555
Gln Ala Ala Thr Glu Val Ala Glu Arg Ala Asp Val Gln Trp Val Glu
          565          570          575
Lys Val Arg Leu Ile Glu Tyr Leu Arg Asn Tyr Ile Ala Ser Arg Leu
          580          585          590
Glu Arg Gly Glu Phe Glu Asn Asn Glu Ser Gly Gly Gly Asn Ser Ser
          595          600          605
Ser Asn Gly Ser Ser His Glu Gln Thr Pro Glu Ala Ser Pro Asp Thr
          610          615          620
His Met Glu Gly Val Glu Ser Glu Val Pro Ser Lys Ala Glu Glu Pro
          625          630          635
Ala Val Lys Pro Glu Ala Gly Asp Val Val Met Tyr Pro Thr Leu Arg
          645          650          655
Ala Val Asp Glu Asp Gly Asp Ser Lys Met Pro
          660          665

```

<210> 3
 <211> 643
 <212> PRT
 <213> Penicillium chrysogenum

```

    <400> 3
Met Thr Glu Asn His Thr Pro Ser Thr Thr Gln Pro Thr Leu Pro Ala
1          5          10          15
Pro Val Ala Glu Ala Ala Pro Ile Gln Ala Asn Pro Ala Pro Ser Ala
20          25          30
Ser Val Thr Ala Thr Ala Ala Ala Thr Ala Ala Val Asn Asn Ala
35          40          45
Pro Ser Met Asn Gly Ala Gly Glu Gln Leu Pro Cys Gln Trp Val Gly

```

50						55						60					
Cys	Thr	Glu	Lys	Ser	Pro	Thr	Ala	Glu	Ser	Leu	Tyr	Glu	His	Val	Cys		
65					70					75					80		
Glu	Arg	His	Val	Gly	Arg	Lys	Ser	Thr	Asn	Asn	Leu	Asn	Leu	Thr	Cys		
				85					90					95			
Gln	Trp	Gly	Thr	Cys	Asn	Thr	Thr	Thr	Val	Lys	Arg	Asp	His	Ile	Thr		
			100					105					110				
Ser	His	Ile	Arg	Val	His	Val	Pro	Leu	Lys	Pro	His	Lys	Cys	Asp	Phe		
		115						120				125					
Cys	Gly	Lys	Ala	Phe	Lys	Arg	Pro	Gln	Asp	Leu	Lys	Lys	His	Val	Lys		
		130				135					140						
Thr	His	Ala	Asp	Asp	Ser	Glu	Ile	Arg	Ser	Pro	Glu	Pro	Gly	Met	Lys		
145				150					155						160		
His	Pro	Asp	Met	Met	Phe	Pro	Gln	Asn	Pro	Arg	Gly	Ser	Pro	Ala	Ala		
			165						170					175			
Thr	His	Tyr	Phe	Glu	Ser	Pro	Ile	Asn	Gly	Ile	Asn	Gly	Gln	Tyr	Ser		
			180					185					190				
His	Ala	Pro	Pro	Pro	Gln	Tyr	Tyr	Gln	Pro	His	Pro	Pro	Pro	Gln	Ala		
		195				200						205					
Pro	Asn	Pro	His	Ser	Tyr	Gly	Asn	Leu	Tyr	Tyr	Ala	Leu	Ser	Gln	Gly		
		210				215					220						
Gln	Glu	Gly	Gly	His	Pro	Tyr	Asp	Arg	Lys	Arg	Gly	Tyr	Asp	Ala	Leu		
225				230					235					240			
Asn	Glu	Phe	Phe	Gly	Asp	Leu	Lys	Arg	Arg	Gln	Phe	Asp	Pro	Asn	Ser		
			245					250						255			
Tyr	Ala	Ala	Val	Gly	Gln	Arg	Leu	Leu	Gly	Leu	Gln	Ala	Leu	Gln	Leu		
		260						265					270				
Pro	Phe	Leu	Ser	Gly	Pro	Ala	Pro	Glu	Tyr	Gln	Gln	Met	Pro	Ala	Pro		
		275						280				285					
Val	Ala	Val	Gly	Gly	Gly	Gly	Gly	Gly	Tyr	Gly	Gly	Gly	Ala	Pro	Gln		
		290				295					300						
Pro	Pro	Gly	Tyr	His	Leu	Pro	Pro	Met	Ser	Asn	Val	Arg	Thr	Lys	Asn		
305				310						315				320			
Asp	Leu	Ile	Asn	Ile	Asp	Gln	Phe	Leu	Glu	Gln	Met	Gln	Asn	Thr	Ile		
			325					330					335				
Tyr	Glu	Ser	Asp	Glu	Asn	Val	Ala	Ala	Ala	Gly	Val	Ala	Gln	Pro	Gly		
		340					345						350				
Ala	His	Tyr	Val	His	Gly	Gly	Met	Asn	His	Arg	Thr	Thr	His	Ser	Pro		
		355				360						365					
Pro	Thr	His	Ser	Arg	Gln	Ala	Thr	Leu	Leu	Gln	Leu	Pro	Ser	Ala	Pro		
		370				375					380						
Met	Ala	Ala	Ala	Thr	Ala	His	Ser	Pro	Ser	Val	Gly	Thr	Pro	Ala	Leu		
385				390						395				400			
Thr	Pro	Pro	Ser	Ser	Ala	Gln	Ser	Tyr	Thr	Ser	Asn	Arg	Ser	Pro	Ile		
			405						410				415				
Ser	Leu	His	Ser	Ser	Arg	Val	Ser	Pro	Pro	His	Glu	Glu	Ala	Ala	Pro		
			420					425					430				
Gly	Met	Tyr	Pro	Arg	Leu	Pro	Ala	Ala	Ile	Cys	Ala	Asp	Ser	Met	Thr		
		435				440					445						
Ala	Gly	Tyr	Pro	Thr	Ala	Ser	Gly	Ala	Ala	Pro	Pro	Ser	Thr	Leu	Ser		
		450				455					460						
Gly	Ala	Tyr	Asp	His	Asp	Asp	Arg	Arg	Arg	Tyr	Thr	Gly	Gly	Thr	Leu		
465				470					475					480			
Gln	Arg	Ala	Arg	Pro	Ala	Glu	Arg	Ala	Ala	Thr	Glu	Asp	Arg	Met	Asp		
			485						490					495			

```

Ile Ser Gln Asp Ser Lys His Asp Gly Glu Arg Thr Pro Lys Ala Met
      500      505      510
His Ile Ser Ala Ser Leu Ile Asp Pro Ala Leu Ser Gly Thr Ser Ser
      515      520      525
Asp Pro Glu Gln Glu Ser Ala Lys Arg Thr Ala Thr Ala Thr Glu
      530      535      540
Val Ala Glu Arg Asp Val Asn Val Ala Trp Val Glu Lys Val Arg Leu
      545      550      555
Leu Glu Asn Leu Arg Arg Leu Val Ser Gly Leu Leu Glu Ala Gly Ser
      565      570      575
Leu Thr Pro Glu Tyr Gly Val Gln Thr Ser Ser Ala Ser Pro Thr Pro
      580      585      590
Gly Leu Asp Ala Met Glu Gly Val Glu Thr Ala Ser Val Arg Ala Ala
      595      600      605
Ser Glu Gln Ala Arg Glu Glu Pro Lys Ser Glu Ser Glu Gly Val Phe
      610      615      620
Tyr Pro Thr Leu Arg Gly Val Asp Glu Asp Glu Gly Asp Ser Lys
      625      630      635      640
Met Pro Glu

```

```

<210> 4
<211> 585
<212> PRT
<213> Yarrowia lipolytica

```

```

<400> 4
Met Ala Ser Tyr Pro Tyr Leu Ala Gln Ser Gln Pro Pro Gln Gln Gln
  1      5      10      15
Gln Gln Gln Gln Gln Pro Gln Gln Gln Ser Gln Gln Leu Pro Thr
  20      25      30
Thr Ala Pro Ser Ala Ala Pro Gln Val Asn Asn Thr Thr Ala Asn Lys
  35      40      45
Pro Leu Tyr Pro Ala Ser Pro Asn Ser Pro Ile Ser Pro Ser Asp Tyr
  50      55      60
Ser Ala Asn Met Asn Val Gly Gly Asp Ser Val Asp Met Leu Leu Ser
  65      70      75      80
Ser Val Ser Ala His His Arg Ser Ser Asp Ala Gly Gln Ser Asp Met
      85      90      95
Gly Ser Ile Ser Pro Ser Thr Ala His Thr Thr Pro Asp Ala Thr Thr
  100      105      110
Tyr Lys Thr Ser Asp Glu Glu Asp Ala Thr Gly Lys Ile Thr Thr Pro
  115      120      125
Arg Ser Glu Gly Ser Pro Asn Thr Asn Gly Ser Gly Ser Asp Gly Glu
  130      135      140
Asn Leu Val Cys Lys Trp Gly Pro Cys Gly Lys Thr Phe Gly Ser Ala
  145      150      155      160
Glu Lys Leu Tyr Ala His Leu Cys Asp Ala His Val Gly Arg Lys Cys
      165      170      175
Thr His Asn Leu Ser Leu Val Cys Asn Trp Asp Asn Cys Gly Ile Val
      180      185      190
Thr Val Lys Arg Asp His Ile Thr Ser His Ile Arg Val His Val Pro
      195      200      205
Leu Lys Pro Tyr Lys Cys Asp Phe Cys Thr Lys Ser Phe Lys Arg Pro
  210      215      220

```

Gln Asp Leu Lys Lys His Val Lys Thr His Ala Asp Asp Asn Glu Gln
 225 230 235 240
 Ala His Asn Ala Tyr Ala Lys Pro His Met Gln His Thr His Gln Gln
 245 250 255
 Gln Gln Gln Gln Gln Arg Tyr Met Gln Tyr Pro Thr Tyr Ala Ser Gly
 260 265 270
 Tyr Glu Tyr Pro Tyr Tyr Arg Tyr Ser Gln Pro Gln Val Gln Val Pro
 275 280 285
 Met Val Pro Ser Tyr Ala Ala Val Gly His Met Pro Thr Pro Pro Met
 290 295 300
 His Pro His Ala Pro Ile Asp Arg Lys Arg Gln Trp Asp Thr Thr Ser
 305 310 315 320
 Asp Phe Phe Asp Asp Ile Lys Arg Ala Arg Val Thr Pro Asn Tyr Ser
 325 330 335
 Ser Asp Ile Ala Ser Arg Leu Ser Thr Ile Glu Gln Tyr Ile Gly Ile
 340 345 350
 Gln Gly Gln Gln Gln Ala Ser Pro Thr Pro Gln Thr Ala Thr Thr
 355 360 365
 Thr Ser Ala Thr Pro Ala Pro Ala Ala Pro His Gln Ala Thr Pro Pro
 370 375 380
 Gln Gln Gln Leu Pro Ser Phe Lys Gln Gly Asp Tyr Gln Glu Thr Asp
 385 390 395 400
 Gln Phe Leu Asn Gln Leu Gly Ser Asn Ile Tyr Gly Asn Ile Lys Ser
 405 410 415
 Val Asp Pro Gln Tyr Glu Ala Pro Ala Glu Phe His Leu Pro His Pro
 420 425 430
 Met Gly Tyr Arg Tyr Ala Phe Ser His Ala Pro Ala Pro His Gly Ala
 435 440 445
 Ala Pro Val Ala Pro Gln Val Ala Pro Pro Ala His Pro Gly Val His
 450 455 460
 Gly Val Ser Ala Pro His Tyr Pro Asp Leu Ser Tyr Ser Arg Ser Thr
 465 470 475 480
 Val Pro Gln Leu Ser Ser Arg Phe Glu Asp Val Arg Gln Met Ser Val
 485 490 495
 Gly Val Thr Gln Arg Ala Ala Arg Thr Thr Asn Val Glu Glu Ser Asp
 500 505 510
 Asp Asp Asp Glu Leu Val Glu Gly Phe Gly Lys Met Ala Ile Ala Asp
 515 520 525
 Ser Lys Ala Met Gln Val Ala Gln Met Lys Lys His Leu Glu Val Val
 530 535 540
 Ser Tyr Leu Arg Arg Val Leu Gln Glu Ala Arg Glu Thr Glu Ser Gly
 545 550 555 560
 Glu Ala Glu Asp Thr Ala Ala Asn Lys Asp Thr Ser Ala Ser Lys Ser
 565 570 575
 Ser Leu Tyr Pro Thr Ile Lys Ala Cys
 580 585

<210> 5
 <211> 659
 <212> PRT
 <213> Candida albicans

<400> 5
 Met Asn Tyr Asn Ile His Pro Val Thr Tyr Leu Asn Ala Asp Ser Asn
 1 5 10 15

Thr Gly Ala Ser Glu Ser Thr Ala Ser His His Gly Ser Lys Lys Ser
 20 25 30
 Pro Ser Ser Asp Ile Asp Val Asp Asn Ala Xaa Ser Pro Ser Ser Phe
 35 40 45
 Thr Ser Ser Gln Ser Pro His Ile Asn Ala Met Gly Asn Ser Pro His
 50 55 60
 Ser Ser Phe Thr Ser Gln Ser Ala Ala Asn Ser Pro Ile Thr Asp Ala
 65 70 75 80
 Lys Gln His Leu Val Lys Pro Thr Thr Thr Lys Pro Ala Ala Phe Ala
 85 90 95
 Pro Ser Ala Asn Gln Ser Asn Thr Thr Ala Pro Gln Ser Tyr Thr Gln
 100 105 110
 Pro Ala Gln Gln Leu Pro Thr Gln Leu His Pro Ser Leu Asn Gln Ala
 115 120 125
 Tyr Asn Asn Gln Pro Ser Tyr Tyr Leu His Gln Pro Thr Tyr Gly Tyr
 130 135 140
 Gln Gln Gln Gln Gln Gln Gln His Gln Glu Phe Asn Gln Pro Ser
 145 150 155 160
 Gln Gln Tyr His Asp His His Gly Tyr Tyr Ser Asn Asn Asn Ile Leu
 165 170 175
 Asn Gln Asn Gln Pro Ala Pro Gln Gln Asn Pro Val Lys Pro Phe Lys
 180 185 190
 Lys Thr Tyr Lys Lys Ile Arg Asp Glu Asp Leu Lys Gly Pro Phe Lys
 195 200 205
 Cys Leu Trp Ser Asn Cys Ser Ile Ile Phe Glu Thr Pro Glu Ile Leu
 210 215 220
 Tyr Asp His Leu Cys Asp Asp His Val Gly Arg Lys Ser Ser Asn Asn
 225 230 235 240
 Leu Ser Leu Thr Cys Leu Trp Glu Asn Cys Gly Thr Thr Thr Val Lys
 245 250 255
 Arg Asp His Ile Thr Ser His Leu Arg Val His Val Pro Leu Lys Pro
 260 265 270
 Phe His Cys Asp Leu Cys Pro Lys Ser Phe Lys Arg Pro Gln Asp Leu
 275 280 285
 Lys Lys His Ser Lys Thr His Ala Glu Asp His Pro Lys Lys Leu Lys
 290 295 300
 Lys Ala Gln Arg Glu Leu Met Lys Gln Gln Lys Lys Glu Ala Lys Gln
 305 310 315 320
 Gln Gln Lys Leu Ala Asn Lys Arg Ala Asn Ser Met Asn Ala Thr Thr
 325 330 335
 Ala Ser Asp Leu Gln Leu Asn Tyr Tyr Ser Gly Asn Pro Ala Asp Gly
 340 345 350
 Leu Asn Tyr Asp Asp Thr Ser Lys Lys Arg Arg Tyr Glu Asn Asn Ser
 355 360 365
 Gln His Asn Met Tyr Val Val Asn Ser Ile Leu Asn Asp Phe Asn Phe
 370 375 380
 Gln Gln Met Ala Gln Ala Pro Gln Gln Pro Gly Val Val Gly Thr Ala
 385 390 395 400
 Gly Ser Ala Glu Phe Thr Thr Lys Arg Met Lys Ala Gly Thr Glu Tyr
 405 410 415
 Asn Ile Asp Val Phe Asn Lys Leu Asn His Leu Asp Asp His Leu His
 420 425 430
 His His His Pro Gln Gln Gln His Pro Gln Gln Gln Tyr Gly Gly Asn
 435 440 445
 Ile Tyr Glu Ala Glu Lys Phe Phe Asn Ser Leu Ser Asn Ser Ile Asp

450
 Met Gln Tyr Gln Asn Met Ser Thr Gln Tyr Gln Gln Gln His Ala Gly
 465 470 475
 Ser Thr Phe Ala Gln Gln Lys Pro Thr Gln Gln Ala Ser Gly Gln Leu
 485 490 495
 Tyr Pro Ser Leu Pro Thr Ile Gly Asn Gly Ser Tyr Thr Ser Gly Ser
 500 505 510
 Ser His Lys Glu Gly Leu Val Asn Asn His Asn Gly Tyr Leu Pro Ser
 515 520 525
 Tyr Pro Gln Ile Asn Arg Ser Leu Pro Tyr Ser Ser Gly Val Ala Gln
 530 535 540
 Gln Pro Pro Ser Ala Leu Glu Phe Gly Gly Val Ser Thr Tyr Gln Lys
 545 550 555
 Ser Ala Gln Ser Tyr Glu Glu Asp Ser Ser Asp Ser Ser Glu Glu Asp
 565 570 575
 Asp Tyr Ser Thr Ser Ser Glu Asp Glu Leu Asp Thr Leu Phe Asp Lys
 580 585 590
 Leu Asn Ile Asp Asp Asn Lys Val Glu Glu Val Thr Ile Asp Gly Phe
 595 600 605
 Asn Leu Lys Asp Val Ala Lys His Arg Glu Met Ile His Ala Val Leu
 610 615 620
 Gly Tyr Leu Arg Asn Gln Ile Glu Gln Gln Glu Lys Glu Lys Ser Lys
 625 630 635 640
 Glu Gln Lys Glu Val Asp Val Asn Glu Thr Lys Leu Tyr Pro Thr Ile
 645 650 655
 Thr Ala Phe

<210> 6
 <211> 625
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 6
 Met Val Pro Leu Glu Asp Leu Leu Asn Lys Glu Asn Gly Thr Ala Ala
 1 5 10 15
 Pro Gln His Ser Arg Glu Ser Ile Val Glu Asn Gly Thr Asp Val Ser
 20 25 30
 Asn Val Thr Lys Lys Asp Gly Leu Pro Ser Pro Asn Leu Ser Lys Arg
 35 40 45
 Ser Ser Asp Cys Ser Lys Arg Pro Arg Ile Arg Cys Thr Thr Glu Ala
 50 55 60
 Ile Gly Leu Asn Gly Gln Glu Asp Glu Arg Met Ser Pro Gly Ser Thr
 65 70 75 80
 Ser Ser Ser Cys Leu Pro Tyr His Ser Thr Ser His Leu Asn Thr Pro
 85 90 95
 Pro Tyr Asp Leu Leu Gly Ala Ser Ala Val Ser Pro Thr Thr Ser Ser
 100 105 110
 Ser Ser Asp Ser Ser Ser Ser Ser Pro Leu Ala Gln Ala His Asn Pro
 115 120 125
 Ala Gly Asp Asp Asp Asp Ala Asp Asn Asp Gly Asp Ser Glu Asp Ile
 130 135 140
 Thr Leu Tyr Cys Lys Trp Asp Asn Cys Gly Met Ile Phe Asn Gln Pro
 145 150 155 160
 Glu Leu Leu Tyr Asn His Leu Cys His Asp His Val Gly Arg Lys Ser

10

Met Gly Thr Asn Ser Val Arg Ile Leu Thr Lys Tyr Pro Lys Ile Leu
 610 615 620
 Val
 625

<210> 7
 <211> 815
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic primer based on Aspergillus nidulans and
 herpes virus

<400> 7
 Met Ser Ser Arg Gly Ala Met Ala Glu Glu Ala Val Ala Pro Val Ala
 1 5 10 15
 Val Pro Thr Thr Gln Glu Gln Pro Thr Ser Gln Pro Ala Ala Ala Gln
 20 25 30
 Val Thr Thr Val Thr Ser Pro Ser Val Thr Ala Thr Ala Ala Ala Ala
 35 40 45
 Thr Ala Ala Val Ala Ser Pro Gln Ala Asn Gly Asn Ala Ala Ser Pro
 50 55 60
 Val Ala Pro Ala Ser Ser Thr Ser Arg Pro Ala Glu Glu Leu Thr Cys
 65 70 75 80
 Met Trp Gln Gly Cys Ser Glu Lys Leu Pro Thr Pro Glu Ser Leu Tyr
 85 90 95
 Glu His Val Cys Glu Arg His Val Gly Arg Lys Ser Thr Asn Asn Leu
 100 105 110
 Asn Leu Thr Cys Gln Trp Gly Ser Cys Arg Thr Thr Val Lys Arg
 115 120 125
 Asp His Ile Thr Ser His Ile Arg Val His Val Pro Leu Lys Pro His
 130 135 140
 Lys Cys Asp Phe Cys Gly Lys Ala Phe Lys Arg Pro Gln Asp Leu Lys
 145 150 155 160
 Lys His Val Lys Thr His Ala Asp Asp Ser Val Leu Val Arg Ser Pro
 165 170 175
 Glu Pro Gly Ser Arg Asn Pro Asp Met Phe Gly Gly Asn Gly Lys
 180 185 190
 Gly Tyr Ala Ala Ala His Tyr Phe Glu Pro Ala Leu Asn Pro Val Pro
 195 200 205
 Ser Gln Gly Tyr Ala His Gly Pro Pro Gln Tyr Tyr Gln Ala His His
 210 215 220
 Ala Pro Gln Pro Ser Asn Pro Ser Tyr Gly Asn Val Tyr Tyr Ala Leu
 225 230 235 240
 Asn Thr Gly Pro Glu Pro His Gln Ala Ser Tyr Glu Ser Lys Lys Arg
 245 250 255
 Gly Tyr Asp Ala Leu Asn Glu Phe Phe Gly Asp Leu Lys Arg Arg Gln
 260 265 270
 Phe Asp Pro Asn Ser Tyr Ala Ala Val Gly Gln Arg Leu Leu Ser Leu
 275 280 285
 Gln Asn Leu Ser Leu Pro Val Leu Thr Ala Ala Pro Leu Pro Glu Tyr
 290 295 300
 Gln Ala Met Pro Ala Pro Val Ala Val Ala Ser Gly Pro Tyr Gly Gly
 305 310 315 320

Gly	Pro	His	Pro	ala	Pro	Ala	Tyr	His	Leu	Pro	Pro	Met	Ser	Asn	Val
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				750					755						

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<223> Synthetic primer based on Aspergillus nidulans

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<211> 30

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<210> 10

<211> 35

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide encoding proline rich motif

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35

<210> 11

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide encoding proline rich motif

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31

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37

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<211> 30

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<211> 678

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<223> Synthetic primer based on *Aspergillus nidulans*

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<210> 24

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<212> DNA

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INTERNATIONAL SEARCH REPORT

 International application No.
 PCT/US98/24975

A. CLASSIFICATION OF SUBJECT MATTER IPC(6) : C07K 14/00; C12N 1/15, 15/63; C12P 21/02 US CL : 435/69.1, 254.11, 320.1; 530/300, 350 According to International Patent Classification (IPC) or to both national classification and IPC		
B. FIELDS SEARCHED Minimum documentation searched (classification system followed by classification symbols) U.S. : 435/69.1, 254.11, 320.1; 530/300, 350 Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) Please See Extra Sheet.		
C. DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	US 5,589,362 A (BUJARD et al) 31 December 1996, see entire document, especially columns 2-14.	1-24
Y	WANG et al. Positive and negative regulation of gene expression in eukaryotic cells with an inducible transcriptional regulator. Gene Therapy. June 1997, Vol. 4, pages 432-441, see entire document, especially pages 432-433.	1-24
Y	GERBER et al. Transcriptional Activation Modulated by Homopolymeric Glutamine and Proline Stretches. Science. 11 February 1994, Vol. 263, pages 808-811, see entire document, especially page 808.	1-24
<input checked="" type="checkbox"/> Further documents are listed in the continuation of Box C. <input type="checkbox"/> See patent family annex.		
* Special categories of cited documents: *A* document defining the general state of the art which is not considered to be of particular relevance *E* earlier document published on or after the international filing date *L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) *O* document referring to an oral disclosure, use, exhibition or other means *P* document published prior to the international filing date but later than the priority date claimed	** later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention *X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone *Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art *A* document member of the same patent family	
Date of the actual completion of the international search 10 FEBRUARY 1999		Date of mailing of the international search report 25 FEB 1999
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. (703) 305-3230		Authorized Officer  TERRY A. MCKELVEY Telephone No. (703) 308-0196

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INTERNATIONAL SEARCH REPORT

International application No.

PCT/US98/24975

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	TILBURN et al. The Aspergillus PacC zinc finger transcription factor mediates regulation of both acid- and alkaline- expressed genes by ambient pH. The EMBO Journal. 04 February 1995, Vol. 14, No. 4, pages 779-790, see entire document, especially page 779.	1-24
Y	O'REILLY et al. A single serine residue at position 375 of VP16 is critical for complex assembly with Oct-1 and HCF and is a target of phosphorylation by casein kinase II. The EMBO Journal. 01 May 1997, Vol. 16, No. 9, pages 2420-2430, see entire document, especially page 2420.	1, 4, 16, 20
Y	HAO et al. Mutation of Phosphoserine 389 Affects p53 Function in Vivo. The Journal of Biological Chemistry. 15 November 1996, Vol. 271, No. 46, pages 29380-29385, see entire document, especially page 29380.	1, 4, 16, 20
Y	US 5,462,862 A (GROENEN et al) 31 October 1995, see entire document, especially columns 1-3.	9-24

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INTERNATIONAL SEARCH REPORT

International application No.
PCT/US98/24975

B. FIELDS SEARCHED

Electronic data bases consulted (Name of data base and where practicable terms used):

APS, DIALOG (biotechnology OneSearch databases):

search terms: chimera?, transcription factor?, activat?, pre-activat?, domain?, truncat?, serine, threonine, alanine, aspartic, glutamic, substitut?, replac?, exchang?, PacC, nidulans, fung?, secondary metabolite?, express?, overexpress?, increas?, enhanc?, penicillin, cephalosporin, lovastatin, compactin, cyclosporin, pneumocandin, echinocandin, DNA binding domain?.